

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 29, 2002, 11:38:48 ; Search time 21.33 Seconds
(without alignments)
2914.665 Million cell updates/sec

Title: US-08-485-355B-50

Perfect score: 3374

Sequence: 1 MGDAGVASQRPNRCGRNV.....GKIARVARRARRARAN 647

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2179	64.6	644	2 A43370	capsid protein - N
2	130	3.9	597	2 B75556	hypothetical prote
3	130	3.9	708	1 QOBBB8	UL80 protein - hum
4	126	3.7	3570	2 T45025	mucin MUC5B, trach
5	125.5	3.7	1269	2 A90267	proteinase related
6	125	3.7	2314	2 T28698	hypothetical prote
7	123.5	3.7	1204	2 C75015	probable pyrolysin
8	123	3.6	886	2 S29605	glycoprotein 350/2
9	122	3.6	1582	2 AC1153	adhesin homolog 1m
10	121.5	3.6	907	1 QOBBE21	membrane antigen g
11	120	3.6	873	2 B75514	penicillin-binding
12	119.5	3.5	889	2 T09055	proteocadherin 68 -
13	119.5	3.5	2271	2 F90073	hypothetical prote
14	119	3.5	1363	2 T43220	insulin-like growt
15	119	3.5	1993	2 AF1450	probable peptidogl
16	119	3.5	2809	2 T30213	G-cadherin - sea u
17	118.5	3.5	3029	2 S76109	hypothetical prote
18	117.5	3.5	609	2 S62518	hypothetical prote
19	117.5	3.5	884	2 E75489	conserved hypothet
20	117.5	3.5	26926	1 T38344	titin, cardiac mus
21	117	3.5	674	2 A97490	hypothetical prote
22	117	3.5	859	2 AE2217	hypothetical prote
23	116	3.4	3716	2 E70969	probable PPE prote
24	115.5	3.4	699	2 A38368	chitinase (EC 3.2.
25	115.5	3.4	3624	2 AD0835	large repetitive p
26	115	3.4	1419	2 T30531	agglutinin-like ad
27	114.5	3.4	710	1 QOBBE22	membrane antigen g
28	114	3.4	828	2 T12184	probable transcrip
29	113.5	3.4	781	1 VCPV19	coat protein VP1 -

30	113	3.3	4436	2 E71086	hypothetical prote
31	112.5	3.3	604	2 A84753	hypothetical prote
32	112	3.3	1090	2 S59077	cellulose 1,4-beta
33	112	3.3	1578	2 AD1512	peptidoglycan boum
34	111.5	3.3	604	2 T31042	hypothetical prote
35	111	3.3	1902	2 B45764	lactocospin (EC 3.4
36	110.5	3.3	505	2 S39962	endoglucanase - Er
37	110.5	3.3	677	2 E75563	probable peptidyl-
38	109.5	3.2	792	2 F88656	protein F56D6.1 [1
39	109.5	3.2	1662	2 T18540	mofta protein precu
40	109	3.2	591	2 B87361	flagellar hook pro
41	109	3.2	766	2 B86597	CT711 hypothetical
42	109	3.2	766	2 F72027	conserved hypothet
43	109	3.2	1302	2 T30191	multidrug resistan
44	108.5	3.2	642	2 B72428	lamininase - The
45	108	3.2	424	2 T32434	hypothetical prote

ALIGNMENTS

RESULT 1

A43370 capsid protein - Nudarelia omega virus

C:Species: Nudarelia omega virus

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999

C:Accession: A43370

R:Agrawal, D. K.; Johnson, J. E.

Virology 190, 806-814, 1992

A:Title: Sequence and analysis of the capsid protein of Nudarelia capensis omega vir

A:Reference number: A43370; MUID:92391097

A:Accession: A43370

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-644 <AGR>

A:Cross-References: GB:S43937

C:Superfamily: Nudarelia omega virus capsid protein

Query Match	64.6%	Score 2179;	DB 2;	Length 644;
Best Local Similarity	64.7%	Pred. No. 2e-145;		
Matches 425;	Conservative 68;	Mismatches 130;	Indels 34;	Gaps 7;
QY	8	SQRPNNRCGRNV	-----SANTVYNGRRNRRCGRQVSPDNFTAAQDLA	57
DB	3	SNSASGRSRNRVRIARQARRARSANVYNAK	-----QRANNIDNTAAQDLG	54
QY	58	QSIDANTVTTPPANISSMPEPRNNAKGI	IDLSDSIGWTKYLDPAGATESARAVGEYSKI	117
DB	55	QSIDANTVTTPPANISSMPEPRNNAKGI	IDLSDSIGWTKYLDPAGATESARAVGEYSKI	114
QY	118	PGSLVFEVDARETIREYNECPVYTDVSVPLDGRQSL	SIFSPMERITVYVANENKE	177
DB	115	PGSLVFEVDARETIREYNECPVYTDVSVPLDGRQSL	SIFSPMERITVYVANENKE	174
QY	178	MSLDVVDNDLIEWLNINLADRWYVDS	EQWINTDTYVYRIRLPTDYVDPPTBGLVNT	237
DB	175	ISLDVVDNDLIEWLNINLADRWYVDS	EQWINTDTYVYRIRLPTDYVDPPTBGLVNT	234
QY	238	VSDYRLTYKATICEANMPTLVDOGF	WIGGOYALTPSLPQYVSEAYALHTLTFARPSSA	297
DB	235	CSDYRLTYKATICEANMPTLVDOGF	WIGGOYALTPSLPQYVSEAYALHTLTFARPSSA	294
QY	298	ALALAFWAGLPQGGTAPACTPAMEQSS	SGGYLTWRNGTTPAGSVSYVLPFGPALERD	357
DB	295	AGYTLTWASMPGGSAPSDPAIIPDSTQF	QWRHGGDAPPGVYTYIIPKQYMWQIFD	353
QY	358	PNDGSWTFASAGDTVTFROVAVDE	VYVYNNPAGGS-----SAPFTTVYV-PPSNAYTNT	411
DB	354	TTTNNNGNFRANDDVVTFQ-----	TGGAAGTNATITTAIPVTLITLITTSAAV	405
QY	412	V-FRNTLTETPRSSRLLELPMPPADFG	QTVANNPKTEGSLKETIGCYLVHSMKRPVFO	470

Db	406	INFRILDAETTHAASNRSEVLPPLRTEGQTAPRNPRIEQTLVKDITGLSTLVHSMKRNPFQ	465
Qy	471	LTPASSFGAVSNPNNGYERTRDLDPYTGIRDSFDONMSTAAVHFSLSHSGSIVTKTQO	530
Db	466	LTPASSFGAISTFTNGEPFRNRLDLPFGGIRDSLDVNMSTAAVCHFSRLSKGSIYTKTQO	525
Qy	531	MEGVNVTMPGQFAGLKNKEITLCADDLATLTGYPATDQFAAASFAFNMSS	590
Db	536	MEGVNVTMPGQFAGHSGLKNDEITLCADDLATLTGYGATDQFAAAYLAFAFNMILTS	585
Qy	591	VLKSEATTSIIKSVETAVGAASGLAKLPGLKMSVPPKIAARVARRARRARAARAN	647
Db	586	VLKSEATTSVKEKELGNOATGLANOGRLAPGLIASIPKIAARVARRARRARRARAARAN	642

RESULT 2

hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: B75556
R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896
A:Accession: B75556
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-597 <WHF>
A:Cross-references: GB:AE001876; GB:AE000513; NID:g6457800; PIDN:AA09732.1; PID:g6457800
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0143
A:Map position: 1

Query Match	3.98;	Score 130;	DB 2;	Length 597;
Best Local Similarity	20.68;	Pred. NO. 0.36;		
Matches 128;	Conservative 67;	Mismatches 253;	Indels 172;	Gaps 25

```

QY 54 ODLAOSLDANVTTPANISSMPEFR-----NNAKKGIDLDSIGFYKFLDPACGT----- 105
Db 4 RDIYDSLPAAPGCGOMVSTSPNYQAVCVNSSGGIISNNSGYNLSLSESSSGSGATVPPA 63
QY 106 -----ESARAVEGEYSKIPDLGVKFSVDAIRE--IYNECP--VYJDLVDPPLDGRQMSLSI 157
Db 64 PTAGATQMSVPGNTIIIPAGTCRFSFDVTLPRAGTYKKNVIANIRIRSGNDADGAQASLTA 123
QY 158 FSPFPEFRAY-----VAVANVEKMSLDV-VNDLIMLNNLADMRIVV 200
Db 124 FAGPVTUKAYPEKSLIDGKATSTLTLTLNNSSPAASVSLAPLDNIC--NGLEITGYTT 181
QY 201 DSEQINFTNTTYVIRIVLRP-----TYDVPDTEGLVTVSDRYLTAYKATCEAMVP 255
Db 182 SCPGATATSGTTIYPSATLNPICITITATVRSKTAG-----SYF 222
QY 256 TLVDOG--FWIGGOYA-----LTPTSLPYDVSEAVV-----LHTLTARPSSA 297
Db 223 NTISAGALQTTVGNNAALASDTLTWTSTRLTITKHAQONFTAGQTGYTVTVASNAGSA 282
QY 298 AALAEVWAGLPOGGIAPRAGTPAMEQASSGYLITMHNHTTPRAGVSIVLPEGFALREXD 357
Db 283 AA-----TSGALSJDLPLSPGMSFNSVT 305
QY 358 PN-DGSWTFASAGDTVTFROVADEVVVTNNPAGGSGAPFTFVAVPVSNAVYTMVFENRT 416
Db 306 TTAGGSFETBRASGAT-----GRVDMFTPTSTPLAAGOSLFTFYVYVNAVNTVANGATLTN 360
QY 417 LLEIRPSSRLLEPMPRPAD-FGQTVYANNPKIEOSLILKETTLCGLYVHSMKRPVOLT--- 472
Db 361 YASVGGGDDPVLLTPPGATCTGEQOCASDPITV-----NRIQTLRLK 402

```

[illegible]

RESULT 3

UB80 protein: human cytomegalovirus (strain Ad169)
 N:contains: capsid assembly protein; viral proteinase (EC 3.4.21.-)
 C:Species: human cytomegalovirus, human herpesvirus 5
 A:Note: host Homo sapiens (man)
 C:Date: 31-Dec-1990 #sequence, revision 31-Dec-1990 #text, change 16-Jul-1999
 C:Accession: S09843; S51034; S51035
 R:Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Hornselli, T
 M.; Barrell, B.G.
 Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
 A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovi
 A:Reference number: S09749; MUID:90269039
 A:Accession: S09843
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-708 <CHE>
 A:Cross-references: EMBL:X17403; NID:959591; PIDN:CA5353.1; PID:91780857
 A:Note: possible protein-coding frames are given
 R:Note: the DNA sequence was submitted to EMBL, December 1989, in computer-readable f
 R:Stevens, J.T.; Mapelli, C.; Tsao, J.; Hall, M.; O'Boyle II, D.; Wehnhemer, S.P.; D
 Bur, J. Biochem. 226, 361-367, 1994
 A:Title: In vitro proteolytic activity and active-site identification of the human cy
 A:Reference number: S51034; MUID:95094793
 A:Accession: S51034
 A:Molecule type: protein
 A:Residues: 110-131, 'X', 133-134 <ST2>
 A:Note: assembly protein release site (Ala-256--Ser-257) and maturation site (Ala-643
 C:Superfamily: cytomegalovirus capsid assembly protein
 C:Keywords: capsid assembly; hydrolase; serine proteinase
 F:1-256/Product: viral proteinase #status predicted <PMAN>
 F:336-708/Product: capsid assembly protein #status predicted <CMP>
 F:137/Active site: Ser #status experimental
 F:256-257/Cleavage site: Ala-Ser (viral proteinase) #status experimental
 F:643-644/Cleavage site: Ala-Ser (viral proteinase) #status experimental

Query Match	3.98;	Score 130;	DB 1;	Length 708;
Best Local Similarity	21.98;	Pred. No. 0.46;		
Matches	89;	Conservative	42;	Mismatches 151;
				Indels 124;
				Gaps 15;

Oy	269	ALPTSLPYQYVNSVAAYL-HITLFARPSMAALAIFVAGLPDGGTAPACNPAEQAISG	327
Dd	319	AESPSTSPSPSEAFASVSHPLSLAIVAAATA-----PPCATYAGASPA---VSS--	364
Oy	328	YLTRHNGHTFPAQSVSYVLPEGFALERYPDNDGSWTDFASAGDTVTFRVAVDEVVNTN	387
Dd	365	-LAMPDHGVYLPKDAFESLL-----	383
Oy	388	NPAGGSAPEFTVEVPENSNATYNTVFENTLTETPRSSRLLEBMP--PADFCGTVANPK	445
Dd	384	----GASSANPVWPCGAVA-----APPASPARPLDPETPSYGAPVVGYDQ	427
Oy	446	IEQSILKETL-----GCIIYSKMKNPNFYOLTPASSFGAASFNNPGYERTDLFD----	495
Dd	428	LAARHFADYVDPHYPGMGRTEREPAPSLHPSTPVPPPS-----PATYRRRDSGGMD	479
Oy	496	-----YTGIIRDSFDQM-----STAVALHRSLSHCISIVTKTYOGWEG	533

Db 480 EPPSGEMRYDGHGHSOKOHRHSGSGCHNRKRRKETAASSSSDEDLSPGFAEHRGAR 539
 QY 534 ---VTWVNPFGFANAGLKNKEILLCLADDLATRLTGVPADNFAAASAFAMMSS 590
 Db 540 KRKSHVNSDGGSGGHAG--SNQOQORDELDALHEL--KRDLEAAQOS--STLLSA 592
 QY 591 VLKSEATSSIIKSVGETAVGAQSLAKLPGILMSVPGKIAARVA 636
 Db 593 ALPSAASSPTTTTCTPTGELTSSGGGERTPALLSGCAVAERAAQ 638

RESULT 4

T45025

mucin MUC5B, tracheobronchial [Imported] - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T45025

R:Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.

J. Biol. Chem. 272, 3168-3178, 1997

A:Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat

A:Reference number: 222899; MUID:97166151

A:Accession: T45025

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-3570 <DES>

A:Cross-references: EMBL:722496; NID:g1834502; PIDN:CAA96577.1; PID:g1834503

A:Experimental source: placenta

C:Genetics:

A:Gene: MUC5B

Query Match 3.7%; Score 126; DB 2; Length 3570;

Best Local Similarity 22.3%; Pred. No. 11;

Matches 94; Conservative 32; Mismatches 178; Indels 118; Gaps 14;

QY 221 LRPTVDPPTGELVTRVSDYRLTY---KATCEANMPTLVDOGFWIGGOYALPTSLP 276
 Db 643 LRSTATPTATSTPTAIPSSILGTTWRLSQTTTPMATST-----ATPSSNP 689
 QY 277 QYVNSAVYALHPTL-----FARSSAAALAFVWAGLPQGGTAPAGCPAMQ 322
 Db 690 E-----TVHTSTVLTATTTGATGATSVATPSSPTGTAHTTKVLTGTTGTAATPSSSP 742
 QY 323 ASSGGYLTWRHNGTTPAGSVSYLPEGFALERYDPNDGSMWDFASAGDTVTRQVAVD 382
 Db 743 GARRLPVM-ISTTTPTTRGSIYVPSST-----PGTHHTPTVLTITT 784
 QY 383 VVVTNNPAGGSAFTTVRVPNSNATNTVFERNLLETRPSSRLLEPMPEADFGQTVAN 442
 Db 785 TVVATGSMATPSSSTQTSPTSLTTATTTATGTTNPSSPTGTPIPPV--LTTTAT 842
 QY 443 NPRIEISLKEITLGCYLVISKMNPFQOLPPASSGAVSFNNNGYERTDLPDYGIRIS 502
 Db 843 TPAATSS-----TVTPSSALGTT-----HTPVPN----- 867
 QY 503 FQGNMSTAAVAFKSLSHS-----CSIYTKYOGMEGVTVNVPFGOFAN-----AGLKN 552
 Db 868 -----TTATTHGRSLSPSSHHTVCTAMTATGATSGILGTHHTESSTGSHRAATTTGTOH 922
 QY 553 EEILCLADLALRLGVPA---TDNFAAASAFAA-----NMSSVLKSEATSSIIK 602
 Db 923 STPALSPHSPSRKTESPSPGTTTGHHTATSRITATAPSKTRSTLLPSQTSAPIT 982
 QY 603 SV 604
 Db 983 TV 984

RESULT 5

A90267

proteinnase related protein [Imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: A90267

R:She, O.; Siroch, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Ch

Jong, T.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder

aretz, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: A90267

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1269 <KUR>

A:Cross-references: GB:AE006641; NID:g13814328; PIDN:AAK41392.1; GSPDB:GN00155

C:Genetics:

A:Gene: SSO1141

Query Match 3.7%; Score 125.5; DB 2; Length 1269;

Best Local Similarity 19.6%; Pred. No. 2.4;

Matches 98; Conservative 69; Mismatches 181; Indels 153; Gaps 27;

QY 18 RNVRVSNVTVNGRRNRRTGRGVSPDNTFAAODLAQSLDANTVTFPANISSMPEF 77
 Db 584 ORLVYANITYPNG-----SPVQ--TGEFKALIENTYLGNTFTTNLTNSLTKL 629
 QY 78 RNWAKGIDLDSDSIGWYFKYLDPAAGATESARAVGEYSKIPGLVKSVDAREIRY--- 134
 Db 630 --WT-GSGVLSKAKSILFVYV--YSSDGLAGIGCYETFEFGYITFNTTTFYVVEL 684
 QY 135 -NECPVTVTVS---VPLDGRQWSLISFSPMERFAYAVAN---VENKESLDVNDL 186
 Db 685 GNAELGITLSNSYFQAPIGVMNITLNIYSNTTNAVTFVTLVSPIKNGVGVIDLPPDL 744
 QY 187 IEMLNLAMRVVNDSEQ--INFMTD--TYVYAIRV-----LRP 223
 Db 745 -----SIGDLLITAEENAGFPAFTNGVYMTFLIPQVYVPGSVSPQHTIGSTIP 799
 QY 224 TVDVPDPT--EGLVTRVSDYRLTYKAITC-----EANNPTLVDOGFWIGGOYALPTSL 275
 Db 800 PNLVSTTFQDALQGT-----NITAKLVSSNGVINEANIP--LSPNGIYRG--YLVIPKMT 852
 QY 276 PQ--YDV-----SEAYALHPTLTPARPSAAL-----AFWAGLPQ 309
 Db 853 PSGLVNVLFAVYSYTLNTTIRGFYGOIYVSNQATISVKSVAFAEGQTFYIANTTN 912
 QY 310 GGA-----PAG-----TPAMQASGGGYLWHRNGT---TFPAGS 342
 Db 913 GTNEIKFGMFSATVYFSSLSFNNTTISLIEIPLMNPKIG--EHEGNFTLPSAISAGN 969
 QY 343 VSVYLPEGFALERYDPNDGSMWDFASAGDTVTRQVAVDVVVTVNPPAGGSAPTFTYV 402
 Db 970 LTVLAGQGYF-----GVPEFK-VLIGISALGNPTTNSGNMYTIVV 1009
 QY 403 PPSNATNTVFERNLLETRPS 423
 Db 1010 LPYTLFTN-----QTLDKTLPS 1026

RESULT 6

T28698

hypothetical protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T28698

R:Parkhill, J.; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, January 1999

A:Reference number: Z20512

A:Accession: T28698

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2314 <PAR>

A:Cross-references: EMBL:AL023496; NID:e1292348; PID:e1292365; PIDN:CAI18915.1

Query Match 3.7%; Score 125; DB 2; Length 2314;
 Best Local Similarity 21.0%; Pred. No. 6.5;
 Matches 157; Conservative 77; Mismatches 252; Indels 260; Gaps 36;

35 ORRRRT--GROVSPPDNFTAAADLAOSLDANTVFPPANISSMPEFRMAKAKIDLDSDSI 92
 Db 979 ERARTVLADSAISPTGTTMAADALRSAYDALTLDEGCAVIAQADPDMEGP-SLVKEA- 1036
 93 GWYFYLDLPAGATESARAVGEYSKIPDGLV-----KFSVDAEIREIY 134
 Db 1037 --YSDGDLGCVTEGAM--QYTLDFGCAVPRSVRYRANSQAQAEPSSVDLHAD-- 1090
 QY 135 NEECPPVTVDSVP-----LDGROMSISIF-- 158
 Db 1091 -ADGPVYATVSLPCTGQNOYTTTVAASDPQALLKASATFVPHASGRQW--VSNFDMY 1148
 QY 159 -----SPPMFRYAVVAANVENK--EMSLDVYNDLEMLN--LADMRVYVSEQ 204
 Db 1149 QFSPEAAPSSPITTLTTLTANTTSTGDSGLPKVSGVFENVTCGAMAEWR----- 1201
 QY 205 WINEFNTTYVYRIRVLRPTVDPPTEGLVRYVSDYRLTYK-----AITCE----- 251
 Db 1202 -----DTDLGDGADJTVSYDKPRS-----RAASDSHIELRPGAKDGPATVPLDYTG 1250
 QY 252 -----ANMPLVDOGFWIGQ--YALTPTSLPQDYSEAVA-LHTLTPAPSSAA----- 298
 Db 1251 SGWCTVASTVRLDPVEEGQDYVAVFVS--TQTDAPYAVNHSLLTRQADAPVFD 1309
 QY 299 ALAFVMAAGLPQGTAPAGTPAMEQASGGYL-----TWRHNGTFFPAGSVSYLVPEGRAL 353
 Db 1310 ATAF-----EGSSGGGLKSEPAWMSGAGSATSLGCT----- 1340
 QY 354 ERYDPDNGSWTDEASAGDYTFEROVADEVVY--NNPA--GGGSAPFTVVRPSPNAYT 409
 Db 1341 -----YCGAMLDY--GD-VDFGDSPKNTVTLTYVNNARSARGTGSAY----- 1378
 QY 410 NTVFRNTLLERPSRRRLLEMPADFGQYVANNPKIEOSLKLKTLCLCYLVHSMKNPVF 469
 Db 1379 -QLTDSFDDPAPGTPTATVPLPT--GSSWSGGTSTLTPAETGTHAHLTLTNAD 1435
 QY 470 QLTP-ASSFGAVSFNNNGEYTRDLPDYTGIRDFQNMSTAVAHFSLSHSCSIYTKY 528
 Db 1436 SSMHYVANTLGOVAFDRVPAQDTL-----SALKKAI 1467
 QY 529 QGMEGVN-----VNPFGQF-----AHAGLKNEELICLADLATR-LGVVPATDNFA 577
 Db 1468 EOYEGLEDEDARYGTIDFGVFRRELTAARDLGTEDATOLEADRTLSLT----- 1517
 QY 578 AAVSAFAANML-----SSVLKSEATSSIIKSVGEVAVGAAGSLAKLPGL 623
 Db 1518 -----LANOLVPLRLRLLESVATASALADERYTDAKMAFTTALTAATLADDETATD 1572
 QY 624 MSVPGKIARVARRA---RRARA 646
 Db 1573 RLLTERAAALDRAASLSLTKRRRTVPA 1598

RESULT 7
 C75015 Probable pyrolysin (EC 3.4.-.-) homolog PAB1252 [similarity] - Pyrococcus abyssi (strain
 A:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: C75015
 R:anonymous, Genoscope
 A:submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: C75015
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-1204 <KAN>
 A:Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:GAB50561.1; PID:g545907
 A:Experimental source: strain Orsay

C:Genetics:
 A:Gene: PAB1252
 C:Keywords: hydrolase

Query Match 3.7%; Score 123.5; DB 2; Length 1204;
 Best Local Similarity 17.4%; Pred. No. 3;
 Matches 145; Conservative 105; Mismatches 261; Indels 323; Gaps 45;

46 PDNFTAAADLAOSLDANTVFPPANISSMPEFRMAKAKIDLDSDSI-----GWYFYLD 100
 Db 237 PENTAMWPNLTQWMA-----PHN-SGNDKMTWQ--LYDSPSSLYNNPCGMVILYLD 288
 QY 101 -----PAGATESARAV--GEYSKIPDGLKFSVDAEIR--EYNECCPVYV 142
 Db 289 NETQWMLKELLYKGYVIGQVAILVLPSEFDYLNHPEDIVG-RLDRIYRLSKNSYSDMWTTG 347
 QY 143 DVSVPDLGRMSLSIFSPFRATYAVVANVENKESLDVNDLI----- 187
 Db 348 DYA-----DMTVARVL-LSMWQYAYSININGRNITPSIELMKDVLTKDFGVSLDDTIPEA 400
 QY 188 -----EMLNINLADMR-----YVVDSEQWINTFND--TTYVYRIRVLRPTDYV 227
 Db 401 VQKINATFYTRFVANNETWMEASFTYSLRGEW--FVNNAFVDIYALLNFMMLIYI 458
 QY 228 PDPT---EGLVRFVSDYRLTYKAITCEANPVL----- 258
 Db 459 PEGTYVKSGRINVI-DELFEYQAMT--GHAIVTIIIGYDDNTTTPDGKALIMVSMGTDWG 516
 QY 259 DQGFWIGQYALNPTSLPQDYSEAVLHITFARP-----SSAALAPV 303
 Db 517 DNGFW--KYS-----KKAARTYHYDRGNPVIYSVRDIISLPFISIGELFVYV 565
 QY 304 -----MAGLPQGTAPAGTPAMEQ--- 322
 Db 566 PKAADYKPLMTVYGKIPYRGEVYDGVNATNVELIYMAQIV--GVAANGSVWHEHSL 624
 QY 323 -----ASSGGLTWNRHNGTFFPAG 341
 Db 625 DFWMYDISDKELSIKONVEIESILPOAHPFDPSPMAFVSEADYIMMEILESNTPL 684
 QY 342 SVS--YVLPPEGFALERY-----DPN-----DGSWT----- 364
 Db 685 TVDFYVAPKDIADNFTGVIYNFTVLNINDELKVLGSLDKNVSTFDGSTVYPLPIPV 744
 QY 365 DFASAGDTVFR---QVADEVVVTNNP---AGGSAPT-----FTVVRPSPNAY 408
 Db 745 SYDKAPNNVTIKYGFDFVSIYSIILEGAKVYVIGKEVPLKAEGGYVYGTETIAKLEL 804
 QY 409 TMTVFRNTLLETTPSSRRLELP-----MPADFGQTVANNPKIE-QSLKET 454
 Db 805 SAGTYNTVTVVTPNGEVALPESRIYVITISGPTIKIVSPV--TVYNNVTIPIEVLVNH 861
 QY 455 LGCYLVHSMKRNVPFOLTPASSFGAVSFNNPGY---ERTRDLDPYIGIRDSFQ--NMGS 509
 Db 862 LKITTNTAIEYGGKSIETL-----YNATS-----GYTGGVYLENGCAVTLVYATDELANNVG 913
 QY 510 AVAHFSLSHSCSIYTKYOGMEGVTVNTPFGQFAHAGLKNEELICLADLATRLT-- 567
 Db 914 ARVHF--VVSANAKVTPVTVEN---TTVT-----VGTGNATITVINDVAVAVTIS 960
 QY 568 -GYV-----PATDFAAASFA-ANMLSSVLKSEATSSIIKSVGEVAVGAAGSG 615
 Db 961 EGYEVKVPVNVN--APALFVNSTAIEDVVKKANATLVAGNNVTVTTRKEVG 1011

RESULT 8
 S29605 glycoprotein 350/220 - human herpesvirus 4
 C:Species: human herpesvirus 4, Epstein-Barr virus
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
 C:Accession: S29605
 R:Klein, K.; Mueller-Lantsch, N.

Query Match	3.6%	Score 123	DB 2	Length 886
Best Local Similarity	20.38%	Pred. No. 2		
Matches 138; Conservative	66;	Mismatches 269;	Indels 206;	Gaps 29;

RESULT 9
AC1153
adhesin homolog Imo0627 [imported] - *Listeria monocytogenes* (strain EGD-e)
C:Species: *Listeria monocytogenes*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC1153
R:Glaser, F.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Dutand, L.; Dussurgeir, O.; Entlian, R.D.; Fsih, H.

Query Match	3.6%	Score 122;	DB 2;	Length 1582;
Best Local Similarity	19.68%	Pred. No. 5.9;		
Matches 122; Conservative	92;	Mismatches 247;	Indels 160;	Gaps 35

RESULT 10
Q0BE21
membrane antigen gp350 - human herpesvirus 4 (strain B95-8)
C.Species: human herpesvirus 4, Epstein-Barr virus
C.Date: 25-Feb-1995 #sequence,revision 25-Feb-1995 #text_change 28-Jul-2000
C.Accession: A43042; S33008; S33009; A03762
R.Bankier, A.T.; Delninger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983

A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
 A:Reference number: A93065; MUID:85035713
 A:Accession: A43042
 A:Molecule type: DNA
 A:Residues: 1-907 <RAN>
 A:Cross-references: GB:V01555; GB:J02070; GB:K01729; GB:K01730; GB:V01554; GB:X00498; GE:R:Farrell, P.J.
 submitted to the EMBL Data Library, March 1988
 A:Reference number: S32973
 A:Accession: S33008
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-907 <PAR>
 A:Cross-references: EMBL:V01555; NID:959074; PIDN:CA24855.1; PID:91334869
 A:Accession: S33009
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-907 <PA2>
 A:Cross-references: EMBL:V01555; NID:959074; PIDN:CA24855.1; PID:91334869
 R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
 Nature 310, 207-211, 1984
 A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
 A:Reference number: A03794; MUID:84270667
 A:Contents: annotation: protein coding region
 C:Superfamily: Epstein-Barr virus membrane antigen gp350

Query Match 3.6%; Score 121.5; DB 1; Length 907;
 Best Local Similarity 19.6%; Pred. No. 2.7;
 Matches 138; Conservative 66; Mismatches 266; Indels 233; Gaps 28;

QY 48 NPTAAADLAQSLDANTVTPPANISSMPEFRNNAKGIKIDDSIGYFYFLDPAGATES 107
 DB 169 NITAVVR--AQGLD--VTPPLSLPTSAODSNFS--VKTEMLG--NEID--IEC 211
 QY 108 ARAVGESKIPDGLVKSVAEIRE-----INNECPVTTDSVPLDGRMSISFSEF 160
 DB 212 IMEDGELSOVLPGDNKNITICSGESHVPSGGLTSTSPVAT--PIGCTGATSLRLTPR 269
 QY 161 PMFR-----TAYVAANVENKEMSLD-----VVNDLI-----EMLNLADMRYVVDSE 203
 DB 270 PVSRLFGNNSILVYFSGNGPKASGDCYCIOSNIVFSDDELPSAGDMPTNTDTIYVGDN- 328
 QY 204 QMNFNTDITTYVIRIRLPTTYDVPDPTBGLVRTVSDYRLTYKAITCEAMPLLVDOGEF 263
 DB 329 -----ATYSVPMTSE-----DANSPVVTYTAFW 352
 QY 264 -----IGGOYALPT----- 273
 DB 353 AMRNNTETDKCKWTLTSGTPSCGENISGAFASNRFTDITVSGLTGAPKTLITRTATNA 412
 QY 274 -----SLPOYDSEAYALHTLTFARPSSAALAFAVAGLPGOGTAPAGPAMEQAS 324
 DB 413 TTTTHKVIKFAPESTTSTPLNTTGFPADPNT-----TGLPSSHYVPTNLTA--PAS 463
 QY 325 SGGYLTRHNGITFPAGSVSYLPEGFALERYDNDGSM-----TDFASAGDIY 373
 DB 464 TGPTVSADVTSPTPAGTSGASP-----VTSPSPMNGTESKAPDMTSTSTSPYTP 516
 QY 374 TFPQVAVDEVVVT-----NNPAGGSAPTFETVAVPPSNAYTNVFR 414
 DB 517 TPNATSTTPAVTTPTPNATSPTPNATSPTLGKTSPTSAVTTTPPNATSPTLGK 576
 QY 415 N-----TLLETPSSRRLELPPPADFCOTVANNPKIEOSLKLKELGICY 458
 DB 577 TSPTSATVTPTPNATSPTLKTSPTS-AVTTTPPNAT-GPTVGETSP-QANATNHTLG-- 631
 QY 459 LVHKKRNPVQLTPASSFEAVSENNNGYERTDLDPYITIRDSFDONMSTAAVHFFSLS 518
 DB 632 ---GTSPPTPVTSQPKNATSAVTTGQ--NHITSSSTSSMSLRPSSNPETLSPSTSDNSTS 686
 QY 519 HSCSIYKTKYQGWEGVNVNTPFGGFHAGLLNNEILCLADLATLTLGVYPAT----- 573

DB 687 HMLPLTSAHPDTGENTITGV--TPASISTH-----HVSTSSPAPRGGTTSQAS 731
 QY 574 --DNFAAVSAPANMLSVLKSEATSSIIKSYGETAVGAQAS 614
 DB 732 GPGNSSTSTPGEVNYTKTTPPNATSPQAPSQCKTAVPIVTS 774

RESULT 11
 B75514
 penicillin-binding protein 1 - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: B75514
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 M.; Shen, M.; Yamachavan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: B75514
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-873 <WHI>
 A:Cross-references: GB:AE001907; GB:AE000513; NID:96458162; PIDN:AAF10059.1; PID:9645
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0479
 A:Map position: 1

Query Match 3.6%; Score 120; DB 2; Length 873;
 Best Local Similarity 26.0%; Pred. No. 3.2;
 Matches 72; Conservative 19; Mismatches 104; Indels 82; Gaps 16;

QY 208 FTNDTTYVYRIRVLR-----PTYDVPDPT-----EGLVTVSDYRL 243
 DB 545 FANGGLYIAPSAVRMEDEPGKVLKRPDPVGRWMDKRYAMGLDMIRGVNDLSAYQ- 603
 QY 244 TYKAITCEANMPTLVDOGEWIGGOYALTPTSILPOYDSEAYALHTLTF--RPSSAALA 301
 DB 604 --GGLATFRARI-----DGMQVCGKGTGT-----NDVKD-----LMFAGVPLDTSGA-- 642
 QY 302 FYWAGLPGGTAP-----GTPAMEQASSGGYLWRHNGTTFPAGSV-----SYLPEGS 350
 DB 643 -VWVGQOEGGTLPSMAYSGEVPPTPVW-QAATAGALAGRETATFIPPGGIYRTYRLNMA 700
 QY 351 FALERYP-----NDGSWTDFASAGDVTTFROVAVDE--VVYTNPPAGGSAP-----T 397
 DB 701 FLTENMDQDPRHRDGS-----RRATXXATTPPAVTAPEPPQATITTPAGGRSPAPLRRRTRR 756
 QY 398 FTVRVPPSNAYTNVFRNTLLETPSSRRLELPPPA 434
 DB 757 LPRQTSFRRLPS-----RTRCPRRPLSPPPRRRPGA 789

RESULT 12
 T09055
 protocadherin 68 - human
 C:Species: *Homo sapiens* (man)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C:Accession: T09055
 R:Jin, P.; Xu, H.; Israel, D.
 submitted to the EMBL Data Library, October 1997.
 A:Reference number: Z16540
 A:Accession: T09055
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-889 <JIN>
 A:Cross-references: EMBL:AF029343; NID:92599501; PID:92599502
 C:Genetics:
 A:Gene: FCH68

us-08-485-355b-50.rpr

```

Query Match      3 58: Score 119.5; DB 2; Length 889;
Best Local Similarity 20.48; Pred. No. 3.6;
Matches 144; Conservative 92; Mismatches 250; Indels 219; Gaps 36;

OY 32 RRNORRRRTGROVSPPDNFTAAQDLSIDANTVFYPANISSMPERRNNAKG----- 83
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 97 RHNAKQGLSLEVFANDKEICIKYIEDINDNAPSFSSQIKLIDISENNAQGRPLTSA 156
OY 84 -KIDLSDSDSIGWYFKYLDPPAGATE-SARAVGEYSKIPDGLKFSVDAEIREIYNECPV 141
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 157 HDPDAGENGRTYLLTRDDHGLFGIDVKSRCGDGTFPELVIOKALD---REQDNHHTLV 213
OY 142 TDVSVPLDEGKOWSLISFSPMFRTAYAVAVANENKEMS-LLVVDNLIEMLNLAQMRV 199
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 214 T-----ALDGE-----PPRSATYQIYNKYIDSDNSVEFPAPSTLVELPENTPIGTIV 262
OY 200 VDSEQWINTFN-----DTTY-----YVIRIYLRPTDYDPDTEGLVTVS--DY----- 241
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 263 ID-----LNATDADGNGEVLVYSSSYVPDRY-RELFSI-DKRTGLIRKGNIDYBNCM 316
OY 242 -----RITYKAIICEANMPTLVDOGFWIGGQALPPTSLPQDYSE 282
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 317 LEIDVQARDIGPNLIIPHACKVTVKLIDRNDAPSI--GF-----VSVRQALSE 363
OY 283 AYALHTLTFEAPRPSAAALAFW---AG-----LPDGGTAPAGTPAMEQASSGGYLT 330
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 364 A-----APGTVIALVRYTDRSGKNGLOQCHVLGGGCTGGGG----- 401
OY 331 WRHNGTTFPAGSVSYVPEGFALERIDPDNSWTFPASAGDVTYTRQV---ANDEVYVTN 387
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 402 ---GIGGPGSGVPEKLEENY-----DNEYT-----VTTDPRMREODEXNVTTI 442
OY 388 NPAGGSGAP-----TFTVRY-----PP-----SNATNTVFRRVTLLETRSSRLEYLPMP 433
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 443 VARDGSGPPLNSTKSFPAIKLIDXNDNPPRFKGLVQLVQHENNI-----PG 488
OY 434 ADGQGYVANNPKTIQ-----SLKETIGCYLVHSHKM-NPYFQLTLPASSFGAVSRNPG 486
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 489 DKLGSVLAQPDQLQNGTVSYSLPSHIGDVSITYVSNP---TNGAIYALRSFN--- 541
OY 487 YERTRDLPDVTGDIRS-----FDQNMSTAVAHFRSLSHSCSIVTKYQCGWEG----- 533
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 542 FEQTKAEFEYVLAKDSQAPAHLESNATYRVTVLYDVNDNAPVTVLPPLQNDTALQVPRNA 601
OY 534 ----VTNVTNPEGQFAHAGLLK-----NEEILCLADLDATRLTGVYPATDN-----F 576
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 602 GLGYLVSTVRALDSDFGESGRLTVEIYDGNDDHLEIPDPSSEIRTLPEFMEDVTPVEL 661
OY 577 AAAVSAFAAMNLSVLSKSEATSSIIKSYGETRAVGAQSLALPLG 621
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 662 VVRVTDHGKPTLSAVAR-----LIIRSVS---GSLPEGVPRVNG 697

RESULT 13
F90073
Hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: F90073
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogunc,
M. A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsutsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F90073
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2271 <KUR>
A:Cross-references: GB:BA000018; PTD:913702612; PIDN:BAB43752.1; GSPDB:GN00149
A:Experimental source: Strain N315
C:Gene: SA2447

```

Query Match Similarity 3.5%; Score 119.5; DB 2; Length 2211; Match Local Similarity 10.9%; Pred. No. 15; Matches 147; Conservative 107; Mismatches 233; Indels 289; Gaps 37;

QY	22	VSANITVTVN-----GRNRORRTGRVSPDPNFTAAODLAOSLANTVTFPPAN	70
Db	254	VTANITITVKNKLLKQYMTTSGNATYDQSTGIVTLTQDAVS-----QKGAITLSTR	303
QY	71	ISSMEFRRWAKGKIDLOS-----DSIGWYK-----	97
Db	304	IDSNKSFH--FSGKYNLKNKYEKGHNGDGDIGAFSPGLGETGLNGAVGIGLSNFG	361
QY	98	-----YLDPAGATSEARAVGEYSKI-----PDGLVKRSY	126
Db	362	EFLDITVHNTSKNSAAKANADPSNAGGARGAFPTTSTGYATTYSSSTADNAAKLV	421
QY	127	-----DAETREIYNEECPVYTDVSVPLDGRQMSLSI-----FSFPM-----	162
Db	422	QPTNNTFODFDIN--YNGDTKVMT--KYAQQVTRNIDPIAKSGTTNPSLWTAAG	476
QY	163	-----FRT--AAYNAANVENKMSLDVNDLI--EMLNLDAMRVNDSQ-----	204
Db	477	GATNIQQVQFGFEETESVTVQRYVDVYTGKDIILPPKTYSGNDQVVYTIIDQOSALTAK	536
QY	205	WNTFTN-DTTYVYVIRIVRLPTDYDPPDEGLRYVSDRLYKATICEANPPLVDQGF	263
Db	537	GKNYTSVDSBY-----ASTYN--DTNKVTMTNAGGSVITYFTFDVNAPIYTVGNQIE	587
QY	264	IGGQVALPPTSLPQDVSEAYALHLLTFARBSAALAFWAGLDQG-----GTAAPGT	317
Db	588	VG--KTMEPVYLTITDNGTGIYNTVT-----GLPSGLSYDSATNSIIGT	630
QY	318	P-----AMEQASSGGYLTWRHN--GTFEPAGSVSYVLPBG--PALERYDP-----	358
Db	631	PKIKQSYVTVYSTQOANNKSTTTFTINVPDTAPT-----VTPIGDQSSSEVYSIPRK	685
QY	359	-----NDGSWTDFAASAGDTVTFROYAVDEVVYNNPAGGSAPTF-----TVRVPSPNAY	408
Db	686	IATQDNGN-----AVTNITVTGLPSGLTPTDSTNNPTISGTPNIG	724
QY	409	TNT-----VFRNTLLETRPSSRLLELMPRADCGQYVANNPKIEQ	448
Db	725	TSTIISIVSTDASGNKTTTTFKYEYTRNSMSDSVSTSGSTQO-----SQSVTSKADSQ	777
QY	449	SLKKEITLGCYLVHSKMRNPVFOLEPPASSFGAVSPN--NGYERTRLDIPYTGIRDSFDQNM	507
Db	778	SASTSTSGIYVS-----TSASTSKTSIVSLSDSVASKSL--TSBSNSVSSST	825
QY	508	STAVAHFNSLSHSCS--IVTKTYQGWEGVYNNVTPGQFAHAGLKNBEI-----	555
Db	826	STSLVNSQSVSSSMGSGVSKSTSLDSISNSNS-----TEKSESLSTSTSLRSTS	876
QY	556	LCIADDLATRLGLGVYPATDNPFAAASAFANLLSLVLSKSEATSTIK--SVGEA	608
Db	877	TSLSDLSKSTISGSLSKSOSTLSISGSS--TSASLSDSTSNKISTSTLSBSA	929

RESULT 14
T43220
Insulin-like growth factor-1 receptor - common lancelet
N:Alternate names: insulin-like peptide receptor
C:Species: Branchiostoma lanceolatum (common lancelet)
C:Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 11-May-2000
C:Accession: T43220
R:Pashmforoush, M.; Chan, S.J.; Steiner, D.F.
Mol. Endocrinol. 10, 857-866, 1996
A:Title: Structure and expression of the insulin-like peptide receptor from amphioxus
A:Reference number: Z2346; MUID:96408719
A:Accession: T43220
A:Molecule type: mRNA
A:Molecule type: translated from GB/EMBL/DBJ

A:Residues: 1-1363 <PAS>
 A:Cross-references: EMBL:SB8394; NID:g1911771; PID:g1911772; PIDN:AAB50848.1
 C:Superfamily: Insulin receptor; protein kinase homology
 C:Keywords: hormone receptor

Query Match 3.58; Score 119; DB 2; Length 1363;
 Best Local Similarity 19.86; Pred. No. 7.6;
 Matches 99; Conservative 60; Mismatches 162; Indels 180; Gaps 23;

```

QY 79 NMAAGKIDLDSDSIGWYK-----YLDPAATESARAVGEYSKIPDGLKFSVDA 128
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 416 DMDTDTIDDGKLFHFHNRKLCRHVLTWADKGLPEHA-----ITD----- 458
QY 129 EIREIYNEECPPVTVDSVPLDGRQWSLIFSFPMEFRTAYAAVANENKESLDVNDLIE 188
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 459 -----TDISTLTGNDQ-----ACSEFSRL-----IE 480
QY 189 WLNLADMRVYVDSQWINFNDTTYVRIYRLVLPDYDVPDPTGGLVRYSDRLTYKAI 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 481 EINTSKMILL---RMSEF-----RP-----DPPRLLSYTVS-YRET----- 514
QY 249 TCEANMPTLVDOGF-WIGQYALPTSLPOYDSEAYALHTLTFARPSSAAL---AFVW 304
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 515 -----EDQIGIDYDGDGACGNTGEMKEDVSPQTAAHITGLKMTQYALLVKITYTK 565
QY 305 AGLPQGG-----TAPAGTPAMEQASSGGYLTMHNGCTTEPPAGSVSYLP 348
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 566 AGAEGSGSAKSDIYARTADKPTHPQDVVYVSSNTLITMKPRNR--PNCNVTHYIV 623
QY 349 EGFALEIYDNDGSMTPDFAAG-----DYTFRQYAVDEYVYVNNPAGGSAPIFTYRVP 403
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 624 K-YKROEDVAEMEQREYCKGGLKPHRPTGLEDIVNNEEPNNSTIGDQTC---CECP 678
QY 404 PS-----NAYNTYFRNTLTETRPSSRLLEPMPAEF--GQTV--- 440
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 679 KSEDEIRIEEBAAFQGEFENFLHNNYHKNRENTRAGRRLRELPTVAREFYSGQTYVNT 738
QY 441 -----ANPKIEOSILKETLCGYLVHSMRN---PVFOLTPASSFGAVSFN 483
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 739 LPSTNRTVPTPTPPNPPOLETTYVNMHM--VVLTLGRHFSEYIIEIVACNADAAVGS 795
QY 484 NPGERTRDLPDYTGIRDSFD 504
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 796 GSAVELARQAD-----DSAD 811

```

RESULT 15
 AFI450
 probable peptidoglycan bound protein (LPXTG motif) 11n0141 [imported] - Listeria innocua
 C:Species: Listeria innocua
 C>Date: 27-Nov-2001 #sequence_rev1sion 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AFI450
 R:Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Magueno, E.; Maltournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tjerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MID:21537279; PMID:11679669
 A:Accession: AFI450
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1993 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CAC95374.1; PID:g16412560; GSPDB:GN00178
 A:Experimental source: strain C1p11262
 C:Genetics:
 A:Gene: 11n0141

Query Match 3.58; Score 119; DB 2; Length 1993;
 Best Local Similarity 19.38; Pred. No. 14;

```

Matches 152; Conservative 100; Mismatches 276; Indels 260; Gaps 38;
QY 3 DAGVASQRPNNRRGTRVRSAMTVYNGRRNCRRTGRQVSPDNDNTAAODLAQSLDA 62
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1247 DASVA-----TAKTLTDGSAIVGSGTN-----GKTRPTD-LTIALKIDIFTEKK 1291
QY 63 NYVTEPANISSMPEFRNMAGKI---DLDSDSIGWYFKYLDPAATESARAVGEYSKIP 118
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1292 STA-----PLYVTANGKVAQKDELKIGATNFTLEKDAVLSL-AQAVTK----- 1336
QY 119 DGLVKSVDALIEIYNEECPPVTVDSVPLDGRQ-----WSLISFPMEFRTAYAAVAN 172
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1337 ---AKTAAFEENKNGVNSDEDEPTD-VKVEQQLAKNGSRGGTYPL---TFLEKN 1389
QY 173 VENKESLID--VYNDLIEWNLNAD-----WRYVVDSEQWINFNDTTYVRIYRLVRL 222
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1390 GKEVEYIDYKVERKDLLE--VNAHDSITYGDMWRADNDSALNKEGETLTFADLEARG 1447
QY 223 P-----TYVDPDPTGGLVRYSDRLTYKAITCEANMPTLVDOGFWT----- 264
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1448 TVDTTRAGEYPTVYKYNDTKVTYTKD-----DATEINAHDSITYGDTWSAKDNFDS 1502
QY 265 -----GGQVALPTPSLPQYDSEAYALHTLTFARPSSAALAFVWAGLPQGGTAPAGTPA 319
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1503 AADRDGNEVALSKVYTVNTVNTAQAGTYPTTY-----YGGVSKITYVT 1546
QY 320 WEQASSGGYLTMHNGCTTEPPAGSVSYLPEGFALERYDNDGSMT---DFASA---GDT 372
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1547 VKENKKG---INAHNMTIYV-----DSMTAEDFNDAVVDGMP 1583
QY 373 VTRQYAVDEVV-VTNPNAG-----GGSAPFTVRY---PSNAYNTYFRNTLLE 419
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1584 VEFKSYVYETPTPVNTNKGATYOLKTYTFDQASATVTLTKNIQTANAHNSYVGEETWE 1643
QY 420 TR---PSSRRLLEPMPADGCTVA--NPKIEOSILKETLGCGLVSK-----M 464
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1644 AKDNFDSARKD-----GETVAPADVEEGNVMTVAGTISTYTKYDGSKITIKVTV 1695
QY 465 RNPVOLTTPASSF-----GAVSFNNGP--- 486
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1696 KNPQTAITAHDSVYVYGDWMSAKDNFDSAIDKAKRPVAYRDITVEEDPTVDINTPTYSV 1755
QY 487 ---YE-----RTRLDPDTG---IRDSFDQ-----NMSTAAVNH 513
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1756 TYKYGGISKVVQITVKPRQTKYESHDSITLYAGSMNAKDNFSDAIDKGDVYKLSOVTVI 1815
QY 514 FRLSHSCSIYTKYQWEGEVNTVPTFGFAHAGLCKNEELCLADDLATRLTGVPAT 573
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1816 GRVNDQTPGYETITR-YGCVTSVSRVYVLQNNAKIIVDSKL-----KINDMDQAK 1866
QY 574 DNFAAASAFANMLSSVLKSEATSSIIKSVGETAV-----GAQSGGLAKL--PGLL 623
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1867 DNFVRAMSRGSEIRPMSKVKVBGKVN-TKKAGYQYTYTIDPNEGTVADGKEELSTVATI 1925
QY 624 MSVPGKIA 631
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1926 EYVEGKVA 1933

```

Search completed: May 29, 2002, 11:40:28
 Job time: 100 sec